

RAW SEQUENCE LISTING DATE: 04/19/2001
PATENT APPLICATION: US/09/435,274A TIME: 14:24:55

Input Set : A:\Cpg.pto
Output Set: N:\CRF3\04192001\I435274A.raw

3 <110> APPLICANT: Citovsky, Vitaly H
4 Rhee, Yoon
6 <120> TITLE OF INVENTION: Genetic Assay for Protein Nuclear Transport
8 <130> FILE REFERENCE: 001.00301
10 <140> CURRENT APPLICATION NUMBER: US 09/435,274A
11 <141> CURRENT FILING DATE: 1999-11-05
13 <150> PRIOR APPLICATION NUMBER: US 60/107,417
14 <151> PRIOR FILING DATE: 1998-11-06
16 <160> NUMBER OF SEQ ID NOS: 13
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 611
22 <212> TYPE: DNA
23 <213> ORGANISM: Unknown Organism
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Description of Unknown Organism:bacterial
28 <220> FEATURE:
29 <223> OTHER INFORMATION: modified bacterial lexA
31 <400> SEQUENCE: 1
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33 cagacaggta tgccggccgac ggggtggaa atcgccgcagg gtttggggtt cgttccccaa 120
34 acggggctga agaacatctg aaggccgtgg cacgc当地agg cggttattgaa attgtttccg 180
35 ggc当地atcagg cgggattcgt ctgttgcagg aagaggaaagg agggttgcgg ctggtaggtc 240
36 gtttggctgc cggtaaccat ctttggcgc aacaggatata tgaaggcat ttttggatc 300
37 atcccccattt attcggccgg aatgtgttattt ttgttgcggc cgttccgggg atgttgttgc 360
38 aagatatccgg cattatggat ggtgacttgc tggcagtgc当地 taaaactcag gatgtacgt 420
39 acgttcaggat ctttgcggcata cgttattgttgc aacggatgttgc ctttggggc ctggaaaaac 480
40 aggccataaa aqtcgaaactg ttgc当地ggaaa ataggcgttgc当地 taaaccattt gtcgttgacc 540
41 ttccgtcaggca gagcttcacc atttgc当地ggc tggcgggttgc ggttatttgc当地 aacggcgttgc 600
42 ggcttggaaattt c 611
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46 <211> LENGTH: 204
47 <212> TYPE: PRT
48 <213> ORGANISM: Unknown Organism
50 <220> FEATURE:
51 <223> OTHER INFORMATION: Description of Unknown Organism:bacterial
53 <220> FEATURE:
54 <223> OTHER INFORMATION: modified bacterial lexA
56 <400> SEQUENCE: 2
57 Met Lys Ala Leu Thr Ala Arg Gln Gln Glu Val Phe Asp Leu Ile Arg
58 1 5 10 15
59 Asp His Ile Ser Gln Thr Gly Met Pro Pro Thr Arg Ala Glu Ile Ala
60 20 25 30
63 Gln Arg Leu Gly Phe Arg Ser Pro Asn Ala Ala Glu Glu His Leu Lys
64 35 40 45
66 Ala Leu Ala Arg Lys Gly Val Ile Glu Ile Val Ser Gly Ala Ser Arg
67 50 55 60

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69 Gly Ile Arg Leu Leu Gln Glu Glu Glu Gly Leu Pro Leu Val Gly
 70 65 70 75 80
 72 Arg Val Ala Ala Gly Glu Pro Leu Leu Ala Cln Gln His Ile Glu Gly
 73 85 90 95
 75 His Tyr Gln Val Asp Pro Ser Leu Phe Lys Pro Asn Ala Asp Phe Leu
 76 100 105 110
 78 Leu Arg Val Ser Gly Met Ser Met Lys Asp Ile Gly Ile Met Asp Gly
 79 115 120 125
 81 Asp Leu Leu Ala Val His Lys Thr Cln Asp Val Arg Asn Gly Gln Val
 82 130 135 140
 84 Val Val Ala Arg Ile Asp Asp Glu Val Thr Val Lys Gly Leu Glu Lys
 85 145 150 155 160
 87 Gln Gly Asn Lys Val Glu Leu Leu Pro Glu Asn Ser Glu Phe Lys Pro
 88 165 170 175
 90 Ile Val Val Asp Leu Arg Gln Gln Ser Phe Thr Ile Glu Gly Leu Ala
 91 180 185 190
 93 Val Gly Val Ile Arg Asn Gly Asp Trp Leu Glu Phe
 94 195 200
 97 <210> SEQ ID NO: 3
 98 <211> LENGTH: 7
 99 <212> TYPE: PRT
 100 <213> ORGANISM: Simian virus 40
 102 <220> FEATURE:
 103 <223> OTHER INFORMATION: Large T antigen NLS
 105 <400> SEQUENCE: 3
 106 Pro Lys Lys Lys Arg Lys Val
 107 1 5
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 111 <211> LENGTH: 17
 112 <212> TYPE: PRT
 113 <213> ORGANISM: Xenopus sp.
 115 <220> FEATURE:
 116 <223> OTHER INFORMATION: nucleoplasmin NLS
 118 <220> FEATURE:
 119 <221> NAME/KEY: VARIANT
 120 <222> LOCATION: (3)..(13)
 121 <223> OTHER INFORMATION: Residues 3 to 13 in Xenopus laevis are Pro Ala Ala
 122 <223> OTHER INFORMATION: Thr Lys Lys Ala Gly Gln Ala Lys
 124 <400> SEQUENCE: 4
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 126 1 5 10 15
 128 Leu
 132 <210> SEQ ID NO: 5
 133 <211> LENGTH: 9
 134 <212> TYPE: PRT
 135 <213> ORGANISM: Human immunodeficiency virus type 1
 137 <220> FEATURE:
 138 <223> OTHER INFORMATION: Rev protein NES
 140 <400> SEQUENCE: 5

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141 Leu Pro Pro Leu Glu Arg Leu Thr Leu
142 1 5
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146 <211> LENGTH: 9
147 <212> TYPE: PRT
148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: Description of Artificial Sequence:nuclear export
152 signal
154 <220> FEATURE:
155 <223> OTHER INFORMATION: mutated NES of pNEAM10
157 <400> SEQUENCE: 6
158 Leu Pro Pro Asp Leu Arg Leu Thr Leu
159 1 5
162 <210> SEQ ID NO: 7
163 <211> LENGTH: 4
164 <212> TYPE: PRT
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: Description of Artificial Sequence:nuclear export
169 signal
171 <220> FEATURE:
172 <223> OTHER INFORMATION: residual NES of pNEARev(delta)3
174 <400> SEQUENCE: 7
175 Leu Pro Pro Leu
176 1
179 <210> SEQ ID NO: 8
180 <211> LENGTH: 26
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: GAL4 primer
190 <400> SEQUENCE: 8
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194 <210> SEQ ID NO: 9
195 <211> LENGTH: 27
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: GAL4 primer
205 <400> SEQUENCE: 9
206 gacggatccc cgggtattcg atctctt 27
209 <210> SEQ ID NO: 10
210 <211> LENGTH: 29
211 <212> TYPE: DNA

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212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: GAL4 primer
220 <400> SEQUENCE: 10
221 gggaaattcga taaageggaa ttaattccc 29
224 <210> SEQ ID NO: 11
225 <211> LENGTH: 27
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: GAL4 primer
235 <400> SEQUENCE: 11
236 gacggatccc cgggttatcg atcttctt 27
239 <210> SEQ ID NO: 12
240 <211> LENGTH: 25
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: mutant lexA primer
250 <400> SEQUENCE: 12
251 ccgtttaaggg cctggaaaaaa caggg 25
254 <210> SEQ ID NO: 13
255 <211> LENGTH: 26
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Description of Artificial Sequence:primer sequence
262 <220> FEATURE:
263 <223> OTHER INFORMATION: selection lexA primer
265 <400> SEQUENCE: 13
266 gtgactggtg aggccctcaac caagtcc 26

VERIFICATION SUMMARY

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L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# :4